

[illegible]

-2-

[illegible]

FIGURE 1

TTTTCACATTCAAATTTGATCATATTATTCATATGTTCTTGAACACAGCTGTTGATGCGA

3301 ----- 3360

L T F K I D H I I H M F L K H V V D A Q

450 460

Intron 7

AAACTATCGCGTATGCTGAAAATGTCTCAACTTTCAATTAAATTTTAAATTTTCAGAAAT

3361 ----- 3420

T I A N

GGAATCTCAATTCTCGAGCAGCGTCTTCTTGAATAGGAAACAATAATGTATCAGTACCG

3421 ----- 3480

G I S I L E Q R L L E I G N N N V S V P

470 480

GAGCGACATATACCATCACATTTCAAAAAATTCGGTCTTCATCAGCCAGTGAGATGTAT

3481 ----- 3540

E R H I P S H F Q K F R R S S A S E M Y

500 510

CCAAAACTACAGAAGAACTGTGATCCGTCCTGAAGACTTCCCAAAGTTCATGCAATTG

3541 ----- 3600

P K T T E E T V I R P E D F P K F M Q L

520 530

CACCAGAAATTTCTATGACTCCCTCAAAAATTTTGCATGCTGTTAAACCTATCGTGTACA

3601 ----- 3660

H Q K F Y D S L K N F A C C *

540

ATATTGCGTGTATATTCCCTCGAAATACGTTTATACTTTTTCGCACGAGTTTTCTCATT

3661 ----- 3720

TTTTCATTGTACTTGTTTTATTTCTCTCCAAAATTTCAGATCTATCCCAAATGTTCTTA

3721 ----- 3780

AATTTAATGTTTTCTACAGATACTCAACACATCTTGTTTCATCTCATCTTGTCTTTTTT

3781 ----- 3840

TTTCAAATATATTCAAGTTCTTTTATAATTTTAATTAATCGAATTAATACATTACAGTAA

3841 ----- 3900

AGAATTTCTGTTGACTATTATTTTATCGCATCCAAATGATTATTCCCTATTGTTCTGAAC

3901 ----- 3960

TTCCAAATTGATCATTTTTTAAACACGCCTCATTAAATTGAAAGTCGTACTTTTAGTCTCG

3961 ----- 4020

AACATGAAGTAAGTTATTTTCTGTGTTCTAAATTCAAAGTGCATTCCAAAAGGACATTG

4021 ----- 4080

ATGAGTTTTTCACGAAAACCGTAATTTTTACAATTTCTTTTCAGTTTTGAAGATGTTTCGAT

4081 ----- 4140

TTCTTTCTCTGTTTGGCGTCACTACTACATTGCTTTGCTGCTTCACTTTATCGAGATT

4141 ----- 4200

TTGCCATCAATGGAGTTCCATCTAGACCGATAGCAGTCTTCATATCATTATCCCTGTATA

4201 ----- 4260

TTGTACTGTTTCAGTATTTTAACTTATCGATTACGTACTATATTCAGTGGTTCACTGTTT

4261 ----- 4320

TCGGTCAATGGGTGACACGTGCTCGACGANNAATTTTCAACGACGCAATCTCCTAGTCA

4321 ----- 4380

CTTATCAACCAAGAGCCCTCACCCATG

4381 ----- 4407

FIGURE 1

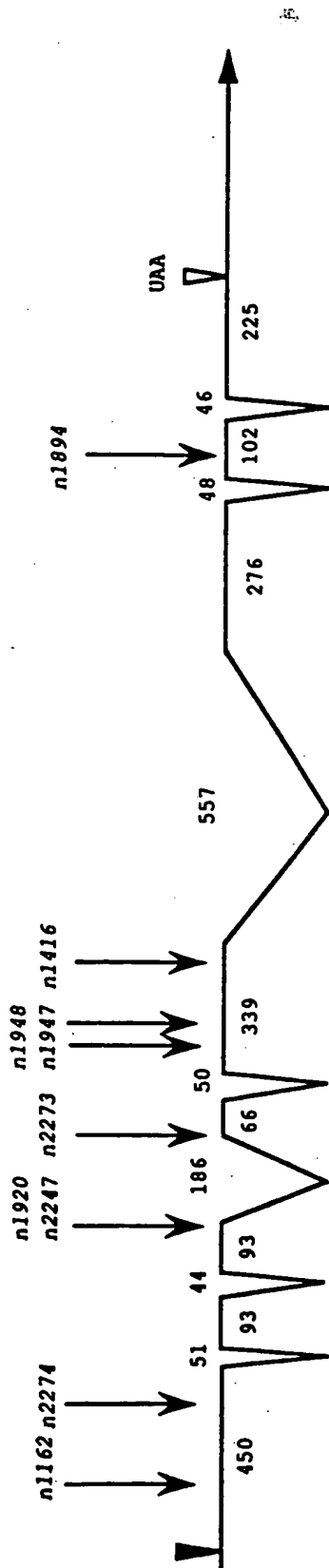


FIGURE 2

09041700Z 021100Z

	10	12	14	18	21
	X	Y	Z	-X	-Z
Calcium-binding loop consensus	D	N	S	T	E
		D	N	S	
			D	E	
				Q	
				D	
				N	
EF-hand consensus	<u>Q * Q * Q G * * Q * * E</u>				
ced-4 sequence 1	Y	N	N	Q	S
sequence 2	S	L	E	I	D
Parvalbumin (carp)	D	Q	D	K	S
(hake)	D	Q	D	K	D
(ray)	D	S	D	G	D
SCBP (<i>Amphioxus I</i>)	D	I	N	K	D
ICaBP (bovine)	A	K	E	G	D
	D	K	N	G	D
Troponin C (rabbit)	D	A	D	G	G
	D	E	D	G	S
	D	R	N	A	D
	D	K	N	N	D
Calmodulin (bovine)	D	K	D	G	N
Trypsinogen	L	G	E	D	N
Fibrinogen	D	N	D	N	D
Villin	G	V	D	P	S
GBP	D	L	N	K	D

FIGURE 3

ced-3 Genomic Sequence

```

1  AGATCTGAAATAAGGTGATAAATTAATAAATTAAGTGTATTTCTGAGGAAATTTGACTGT 60
   -----+-----+-----+-----+-----+
61  TTTAGCACAATTAATCTTGTTTCAGAAAAAAGTCCAGTTTCTAGATTTTCCGCTCTTA 120
   -----+-----+-----+-----+-----+
121  TTGTCGAATTAATATCCCTATTATCACTTTTTCATGCTCATCCTCGAGCGGCACGTCCTC 180
   -----+-----+-----+-----+-----+
181  AAAGAATTGTGAGAGCAAACGCGCTCCCATTTGACCTCCACACTCAGCCGCCAAAACAAAC 240
   -----+-----+-----+-----+-----+
241  GTTCGAACATTCGTGTGTTGTGCTCCTTTCCGTTATCTTGCACTCATCTTTTGTGCTTT 300
   -----+-----+-----+-----+-----+
301  TTTTCTTTGTTCTTTTGTGAACGTGTTGCTAAGCAATTATTACATCAATTGAAGAAAA 360
   -----+-----+-----+-----+-----+
361  GGCTCGCCGATTATTGTTGCCAGAAAGATTCTGAGATTCTCGAAGTCGATTTTATAATA 420
   -----+-----+-----+-----+-----+
421  TTTAACCTTGGTTTTTGCATTGTTTCGTTTAAAAAAACCAGTGTATGTGAAAAACGAT 480
   -----+-----+-----+-----+-----+
481  TAGTTTACTAATAAAACTACTTTTAAACCTTTACCTTTACCTCACCGCTCCGTGTTTCATG 540
   -----+-----+-----+-----+-----+
541  GCTCATAGATTTTTCGATACTCAAATCCAAAAATAAATTTACGAGGGCAATTAATGTGAAA 600
   -----+-----+-----+-----+-----+
601  CAAAAACAATCCTAAGATTTCCACATGTTTGACCTCTCCGGCACCTTCTTCCTTAGCCCC 660
   -----+-----+-----+-----+-----+
661  ACCACTCCATCACCTCTTTGGCGGTGTTCTTCGAAACCCACTTAGGAAAGCAGTGTGTAT 720
   -----+-----+-----+-----+-----+
721  CTCATTTGGTATGCTCTTTTCGATTTTATAGCTCTTTGTGCAATTTCAATGCTTTAAAC 760
   -----+-----+-----+-----+-----+
781  AATCCAAATCGCATTATATTTGTGCATGGAGGCAAATGACGGGGTTGGAATCTTAGATGA 840
   -----+-----+-----+-----+-----+
841  GATCAGGAGCTTTAGGGTAAACGCCCGGTTTATTTGTACCACATTTTCATCTTTTCT 900
   -----+-----+-----+-----+-----+
901  GTCGTCCTTGGTATCCTCAACTTGTCCTGGTTTTGTTTTCGGTACACTCTTCCGTGATGC 960
   -----+-----+-----+-----+-----+
961  CACCTGTCTCCGTCTCAATTATCGTTTAGAAATGTGAACGTCCAGATGGGTGACTCATA 1020
   -----+-----+-----+-----+-----+
1021  TTGCTGCTGTACAATCCACTTTCTTTCTCATCGGCAGTCTTACGAGCCCATCATAAAC 1080
   -----+-----+-----+-----+-----+
1081  TTTTTTTTCCGCGAAATTTGCAATAAACCGGCCAAAAACTTCTCCAAATTGTTACGCAA 1140
   -----+-----+-----+-----+-----+
1141  TATATACAATCCATAAGAATATCTTCTCAATGTTTATGATTCTTCGCAGCACTTTCTCT 1200
   -----+-----+-----+-----+-----+
1201  TCGTGTGCTAACATCTTATTTTATAATATTTCCGCTAAAATTCCGATTTTGTAGTATTA 1260
   -----+-----+-----+-----+-----+
1261  ATTTATCGTAAAATTATCATAATAGCACCGAAAACCTACTAAAAATGGTAAAAGCTCCTTT 1320
   -----+-----+-----+-----+-----+

                                     Repeat 1
                                     -----
1321  TAAATCGGCTCGACATTATCGTATTAAGGAATCACAAAATTCTGAGAATGCGTACTGCGC 1380
   -----+-----+-----+-----+-----+

-----
1381  AACATATTTGACGGCAAATATCTCGTAGCGAAACTACAGTAATTCTTTAAATGACTAC 1440
   -----+-----+-----+-----+-----+

                                     Repeat 1
                                     ----->
1441  TGTAGCGCTTGTGTCGATTTACGGGCTCAATTTTGAAAATAATTTTTTTTTTCGAATTT 1500
   -----+-----+-----+-----+-----+

```

FIGURE 4

[illegible]

FIGURE 4

2581 TTTTAAAGTTCGGCGCAAAAGCAAGGGTCTCACGGAAAAAGAGGCGGATCGTAATTTT 2640
 -----+-----+-----+-----+-----+
 GCAACCCACCGGCACGGTTTTTCTCCGAAATCGGAAATTATGCACTTTCCCAAATAT 2700
 2641 -----+-----+-----+-----+-----+
 TTGAAGTGAAATATATTTTACTGAAAGCTCGAGTGATTATTTATTTTAACTA 2760
 2701 -----+-----+-----+-----+-----+
 ATTTTCGTGGCGCAAAAGGCCATTTGTAGATTGCGGAAATACTTGTACACACACAC 2820
 2761 -----+-----+-----+-----+-----+

 2821 ACACACATCTCCTTCAAATATCCCTTTTTCCAGTGTGACTCGAATGCTGTGAATTCTGA 2880
 -----+-----+-----+-----+-----+
 V D S N A V E F E
 100
 2881 GTGTCCAATGTCACCGGCAAGCCATCGTCGGAGCCGCGCATTGAGCCCCGCGGCTACAC 2940
 -----+-----+-----+-----+-----+
 C P M S P A S H R R S R A L S P A G Y T
 110 120
 2941 TTCACCGACCCGAGTTACCGTGACAGCGTCTCTTCAGTGTCACTTCATTCTTATCA 3000
 -----+-----+-----+-----+-----+
 S P T R V H R D S V S S V S S F T S Y Q
 130 140
 3001 GGATATCTACTCAAGAGCAAGATCTCGTTCTCGATCGCGTCACTTCATTTCATCGGATCG 3060
 -----+-----+-----+-----+-----+
 D I Y S R A R S R S R S R A L H S S D R
 150 160
 3061 ACACAATTATTCATCTCCTCCAGTCAACGCATTTCCAGCCAACCTTGATGTTGATGCG 3120
 -----+-----+-----+-----+-----+
 H N Y S S P P V N A F P S Q P S
 170
 intron 3
 Repeat 1
 3121 AACACTAAATTCTGAGAATGCGCATTACTCAACATATTTGACGCGCAAATATCTCGTAGC 3180
 -----+-----+-----+-----+-----+
 3181 GAAAAATACAGTAACCCTTTAAATGACTATTGTAGTGTGATTACGGGCTCGATTTTCG 3240
 -----+-----+-----+-----+-----+
 -->
 3241 AAACGAATATATGCTCGAATTGTGACAACGAATTTTAATTTGTCATTTTGTGTTTTCTT 3300
 -----+-----+-----+-----+-----+
 Repeat 1
 <-----
 3301 TTGATATTTTGTATCAATTAATAAATTATTTCCGTAAACAGACACCAGCGCTACAGTACT 3360
 -----+-----+-----+-----+-----+
 3361 CTTTAAAGAGTTACAGTAGTTTTCGCTTCAAGATATTTGAAAAGAATTTTAAACATTT 3420
 -----+-----+-----+-----+-----+
 3421 TGAAAAAAATCATCTAACATGTGCCAAAACGCTTTTTTCAAGTTTCGCAGATTTTGTGA 3480
 -----+-----+-----+-----+-----+

FIGURE 4

[illegible]

-4-

4321 TCACCGGATGCTCTTCTCTCGGATACAGTTCAAGTCGTAATCGCTCATTAGCAAAGCTT 4380
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 T G C S S L G Y S S S R N R S F S K A S
 190 200
 4381 CTGGACCAACTCAATACATATTCCATGAAGAGGATATGAACTTTGTCGATGCACCAACCA 4440
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 G P T Q Y I F H E E D M N F V D A P T I
 210 220
 4441 TAAGCCGTGTTTTTCGACGAGAAAACCATGTACAGAACTTCTCGAGTCCTCGTGAATGT 4500
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 S R V F D E K T M Y R N F S S P R G M C
 230 240
 4501 GCCTCATCATAAATAATGAACACTTTGAGCAGATGCCAACACGGAATGGTACCAAGGCCG 4560
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 L I I N N E H F E Q M P T R N G T K A D
 250 260
 4561 ACAAGGACAATCTTACCAATTTGTTTCAGATGCATGGGCTATACGGTTATTTGCAAGGACA 4620
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 K D N L T N L F R C M G Y T V I C K D N
 270 280
 | intron 4
 4621 ATCTGACGGGAAGGGTACGGCGAAATTATATTACCCAAACGCGAAATTTGCCATTTTGGC 4680
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 L T G R
 Repeat 3
 ----->
 4681 CCGAAAATGTGGCGCCCGTCTCGACACGACAATTTGTGTTAAATGCAAAAATGTATAAT 4740
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4741 TTTGCAAAAACAAAATTTTGAACCTCCGCGAAAATGATTTACCTAGTTTCGAAATTTTC 4800
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4801 GTTTTTTCCGGCTACATTATGTGTTTTTCTTAGTTTTTCTATAATATTTGATGTAAAAA 4860
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4861 ACCGTTTGTAATTTTCAGACAATTTTCCGCATACAAAACCTTGATAGCAGCAATCAATT 4920
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4921 TTCTGAATTTTCAAAATTATCCAAAATGCACAATTTAAAATTTGTGAAAATTGGCAAAC 4980
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4981 GGTGTTTCAATATGAAATGTATTTTTTAAAACTTTAAAAACCACTCCGAAAAGCAATAA 5040
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5041 AAATCAAAACAACGTCACAATTCAAATTCAAAAGTTATTCATCCGATTGTTTATTTTGT 5100
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5101 CAAAATTTGAAAAATCATGAAGGATTTAGAAAAGTTTTATAACATTTTTTCTAGATTTT 5160
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5161 TCAAAATTTTTTTTAAACAAATCGAGAAAAAGAGAATGAAAATCGATTTTAAAAATATCC 5220
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 Repeat 3
 <-----
 5221 ACAGCTTCGAGAGTTTGAAATTACAGTACTCCTTAAAGGCGCACACCCCATTTGCATTGG 5280
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

 5281 ACCAAAAATTTGTCGTGTCGAGACCAGGTACCGTAGTTTTTGTGCAAAAATTGCACCAT 5340
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5341 TGGACAATAAACCTTCCTAATCACCAAAAAGTAAAATTGAAATCTTCGAAAAGCCAAAAA 5400
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

FIGURE 4

5401 ATTCAAAAAAAAAAGTCGAATTTTCGATTTTTTTTTTGGTTTTTTGGTCCCAAAAACCAAAA 5460
 -----+-----+-----+-----+-----+-----+-----+-----+
 5461 AAATCAATTTTCTGCAAAATACCAAAAAGAAACCCGAAAAAATTTCCAGCCTTGTTCCT 5520
 -----+-----+-----+-----+-----+-----+-----+-----+
 5521 AATGTAAACTGATATTTAATTTCCAGGGAATGCTCCTGACAATTCGAGACTTTGCCAAAC 5580
 -----+-----+-----+-----+-----+-----+-----+-----+
 G M L L T I R D F A K H
 290 300
 5581 ACGAATCACACGGAGATTCTGCGATACTCGTGATTCTATCACACGGAGAAGAGAATGTGA 5640
 -----+-----+-----+-----+-----+-----+-----+-----+
 E S H G D S A I L V I L S H G E E N V I
 310 320
 5641 TTATTGGAGTTGATGATATACCGATTAGTACACACGAGATATATGATCTTCTCAACGCGG 5700
 -----+-----+-----+-----+-----+-----+-----+-----+
 I G V D D I P I S T H E I Y D L L N A A
 330 340
 A(n2433)
 5701 CAAATGCTCCCGTCTGGCGAATAAGCCGAAAATCGTTTTTGTGCAGGCTTGTTCGAGGCG 5760
 -----+-----+-----+-----+-----+-----+-----+-----+
 N A P R L A N K P K I V F V Q A C R G E
 350 360
 intron 5
 5761 GTTCGTTTTTTATTTTAATTTTAATATAAAATATTTTAAATAAAATTCATTTTCAGAACGTC 5820
 -----+-----+-----+-----+-----+-----+-----+-----+
 R R
 5821 GTGACAATGGATTCCAGTCTTGGATTCTGTGACGGAGTTCCTGCATTTCTTCGTCGTG 5880
 -----+-----+-----+-----+-----+-----+-----+-----+
 D N G F P V L D S V D G V P A F L R R G
 370 380
 T(n1165)
 5881 GATGGGACAATCGAGACGGGCCATTGTTCAATTTTCTTGGATGTGTGCGGCCGCAAGTTC 5940
 -----+-----+-----+-----+-----+-----+-----+-----+
 W D N R D G P L F N F L G C V R P Q V Q
 390 400
 intron 6
 5941 AGGTTGCAATTTAATTTCTTGAATGAGAATATTCCTTCAAAAAATCTAAAATAGATTTTT 6000
 -----+-----+-----+-----+-----+-----+-----+-----+
 6001 ATTCCAGAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC 6060
 -----+-----+-----+-----+-----+-----+-----+-----+
 Repeat 4
 6061 AAACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA 6120
 -----+-----+-----+-----+-----+-----+-----+-----+
 ----->
 6121 GTGAATTGCTGATTGGTCGCAGTTTTTCAGTTTAGAGGGAATTTAAAAATCGCCTTTTCGA 6180
 -----+-----+-----+-----+-----+-----+-----+-----+
 6181 AAATTAATAATGATTTTTTCAATTTTTTCGAAAAATATTCGATTATTTTATATTCTTT 6240
 -----+-----+-----+-----+-----+-----+-----+-----+

FIGURE 4

A(n717)
|

6241 GGAGCGAAAGCCCCGTCCTGTAAACATTTTAAATGATAATTAATAAATTTTGCAGCAA 6300
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
Q

T(n1949)
|

6301 GTGTGGAGAAAGAAGCCGAGCCAAGCTGACATTCTGATTTCGATACGCAACGACAGCTCAA 6360
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
V W R K K P S Q A D I L I R Y A T T A Q
410 420

A(n1286)
|

6361 TATGTTTCGTGGAGAAACAGTGCTCGTGGATCATGGTTCATTCAAGCCGTCTGTGAAGTG 6420
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
Y V S W R N S A R G S W F I Q A V C E V
430 440

T(n1129,n1164)
|

6421 TTCTCGACACACGCAAAGGATATGGATGTTGTTGAGCTGCTGACTGAAGTCAATAAGAAG 6480
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
F S T H A K D M D V V E L L T E V N K K
450 460

T(n2430) | A(n2426) | | intron 7

6481 GTCGCTTGTGGATTTTCAGACATCACAGGGATCGAATATTTTGAAACAGATGCCAGAGGTA 6540
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
V A C G F Q T S Q G S N I L K Q M P E
470 480

Repeat 5

6541 CTTGAAACAAACAATGCATGTCTAACTTTTAAGGACACAGAAAAATAGGCAGAGGCTCCT 6600
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
----->

6601 TTTGCAAGCCTGCCGCGCTCAACCTAGAATTTTAGTTTTTAGCTAAATGATTGATTTT 6660
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
6661 GAATATTTTATGCTAATTTTTTGGCTTAAATTTTGAAATAGTCACTATTTATCGGGTTT 6720
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
6721 CCAGTAAAAAATGTTTATTAGCCATTGGATTTTACTGAAAACGAAAATTTGTAGTTTTTC 6780
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
6781 AACGAAATTTATCGATTTTAAATGTAAAAAATAGCGAAAATTACATCAACCATCAA 6840
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
6841 GCATTTAAGCCAAAATTGTAACTCATTAAAAAATTAATTCAAAGTTGTCCACGAGTATT 6900
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
-----<

Repeat 5

6901 ACACGGTTGGCGCGCGCAAGTTTGCAAAACGACGCTCCGCCTCTTTTCTGTGCGGCTT 6960
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

T(n1163)
|

6961 GAAAACAAGGGATCGGTTTAGATTTTCCCAAAATTTAAATTAAATTTTCAGATGACATC 7020
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
M T S

FIGURE 4

7021 CCGCCTGCTCAAAAAGTTCTACTTTTGGCCGGAAGCACGAAACTCTGCCGTCTAAAATTC 7080
 -----+-----+-----+-----+-----+
 R L L K K F Y F W P E A R N S A V *
 490 500
 7081 ACTCGTGATTCAATTGCCCAATTGATAATTGTCTGTATCTTCTCCCCCAGTTCTCTTTTCGC 7140
 -----+-----+-----+-----+-----+
 7141 CCAATTAGTTTAAACCATGTGTATATTGTTATCCTATACTCATTTCACCTTATCATTCT 7200
 -----+-----+-----+-----+-----+
 7201 ATCATTCTCTTCCCATTTCACACATTTCATTCTCTACGATAATCTAAAATTATGAC 7260
 -----+-----+-----+-----+-----+
 7261 GTTTGTGTCTCGAACGCATAATAATTTTAATAACTCGTTTGAATTTGATTAGTTGTTGT 7320
 -----+-----+-----+-----+-----+
 7321 GCCCAGTATATATGTATGTACTATGCTTCTATCAACAAAATAGTTTCATAGATCATCACC 7380
 -----+-----+-----+-----+-----+
 7381 CCAACCCACCAACCTACCGTACCATATTTCATTTTGGCCGGAATCAATTCGATTAATT 7440
 -----+-----+-----+-----+-----+
 7441 TTAACCTATTTTTCGCCACAAAAATCTAATATTTGAATTAACGAATAGCATTCCCATC 7500
 -----+-----+-----+-----+-----+
 7501 TCTCCCGTGCCGGAATGCCTCCCGGCCTTTTAAAGTTCGGAACATTTGGCAATTATGTAT 7560
 -----+-----+-----+-----+-----+
 7561 AAATTTGTAGGTCCCCCCCATCATTTCCCGCCCATCATCTCAAATTGCATTCTTTTTTCG 7620
 -----+-----+-----+-----+-----+
 7621 CCGTGATATCCCGATTCTGGTCAGCAAAGATCT 7653
 -----+-----+-----+-----+-----+

FIGURE 4

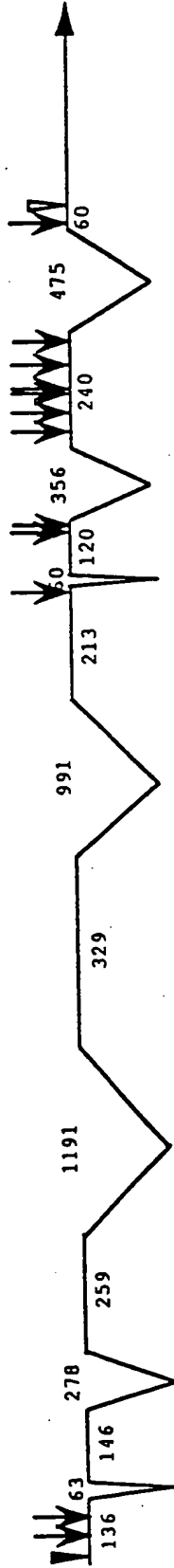


FIGURE 5A

ced-3 Mutations are Clustered

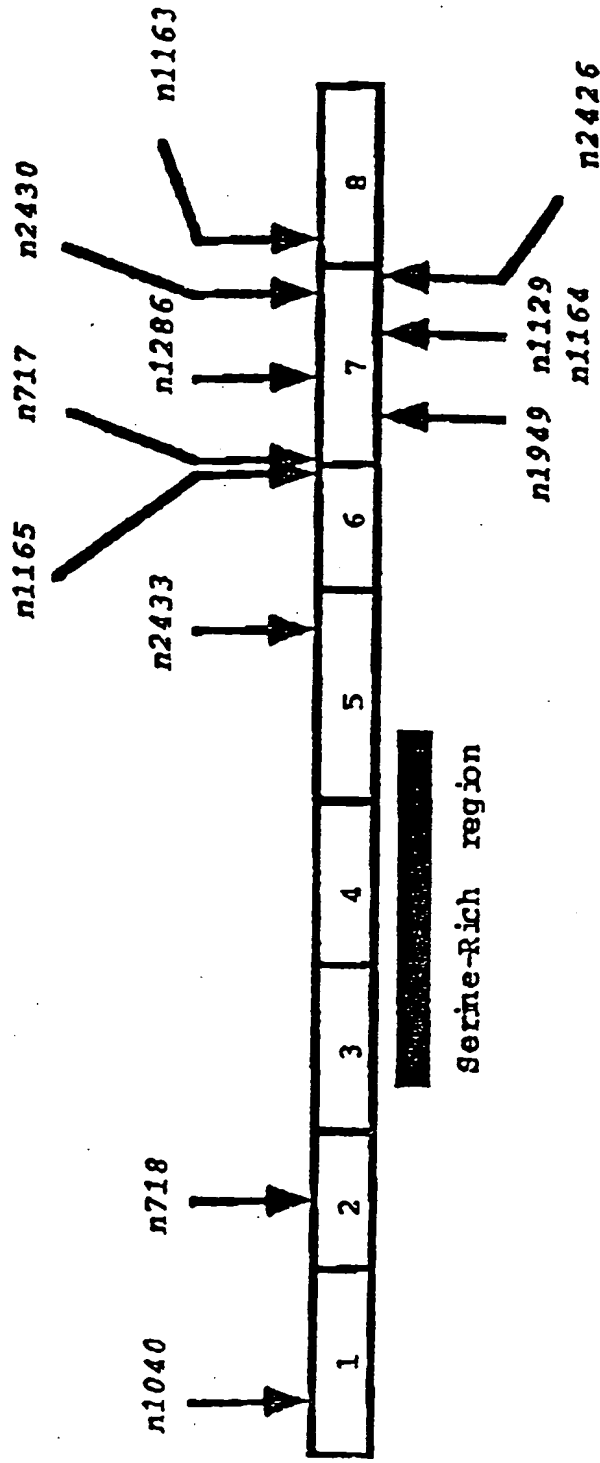


FIGURE 5B

080341Z FEB 68

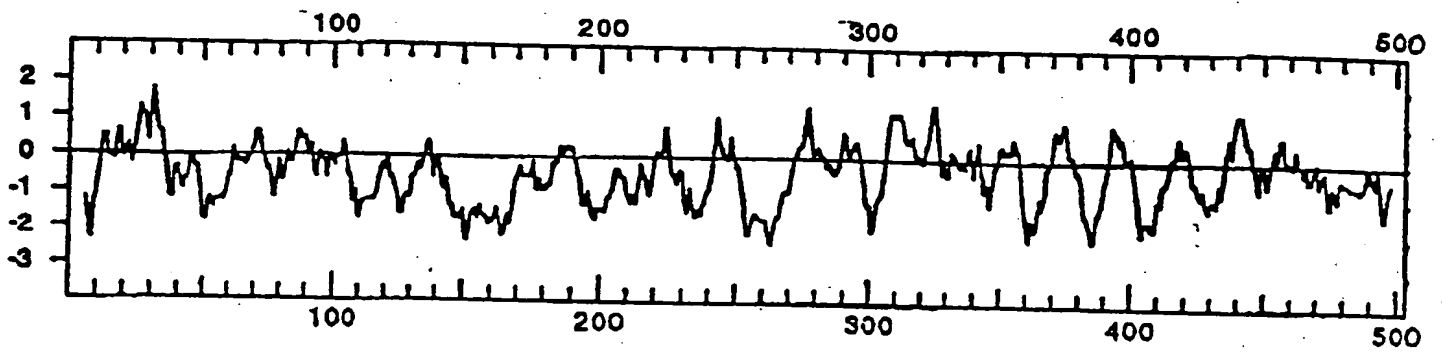


FIGURE 6

1	01	MMQDRRSLLERNIMMFSSHLKVDEILEVLIAKQVLNSDNGDMINSCGTV	50
2	W.....LE...K.QA.L..D.....V....R.E	
3		TVS\SLI..R.....M.....	
1	51	REKRREIVKAVQRPQDVAFDAFYDALRSTGHEGLAEVLEPLARSVDSNAV	100
2		.DNEK.....R..E.....D...ND..D..M..S.P..P.	
3			
1	101	EFECPMSPASHRRSRALSPAGYTSPTVRHRDSVSSVSSTS_YQDIYSRA	149
2		PM.....S.....P..A.....I.....T...V....	
3			S
1	150	RSRSR_SRALHSSDRHNYSSPPVNAFSPQSSANSSTGCSLGYSSSRN	198
2		..S...S...P.Q.....M.AA_TS.....A.....	
3		T...__..P..T.....V..S..S.Q...A.....S.....T	
1	199	RSFSKASGPTQYIFHEEDMNFVDAPTISRVFDEKTMYNFSSPRGMCLI	247
2	T.AQS.....Y.....H.....L...	
3		..Y....AHS.....Y.....H.....T...L...	
1	248	INNEHFQMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRD	297
2	I.....E..S...S	
3	P....IS.....I.H.....M.....	
1	298	FAKHESHGDSAILVILSHGEENVIIGVDDIPISTHEIYDLLNAANAPRLA	347
2		.GRNDM.....VSVNV.....	
3		...N.T.....VSVNV....X.....	
1	348	NKPKIVFVQACRGERRDNGFPVLDSDVGVP AFLRRGWDNRDGPLFNFLGC	397
2	L.....SLI.....	
3	L.....V.....LI.....KG.....	
1	398	VRPQVQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVCEVFST	447
2	M..A.....L	
3	A.....A.....L	
1	448	HAKDMDVVELLTEVNKKVACGFQTSQGSNILKQMPMTSRLKKFYFWPE	497
2	L.....	
3	A.....L.....	
1	498	ARN SAV 503	
2		DRG.....	
3		D..RS...	

FIGURE 7

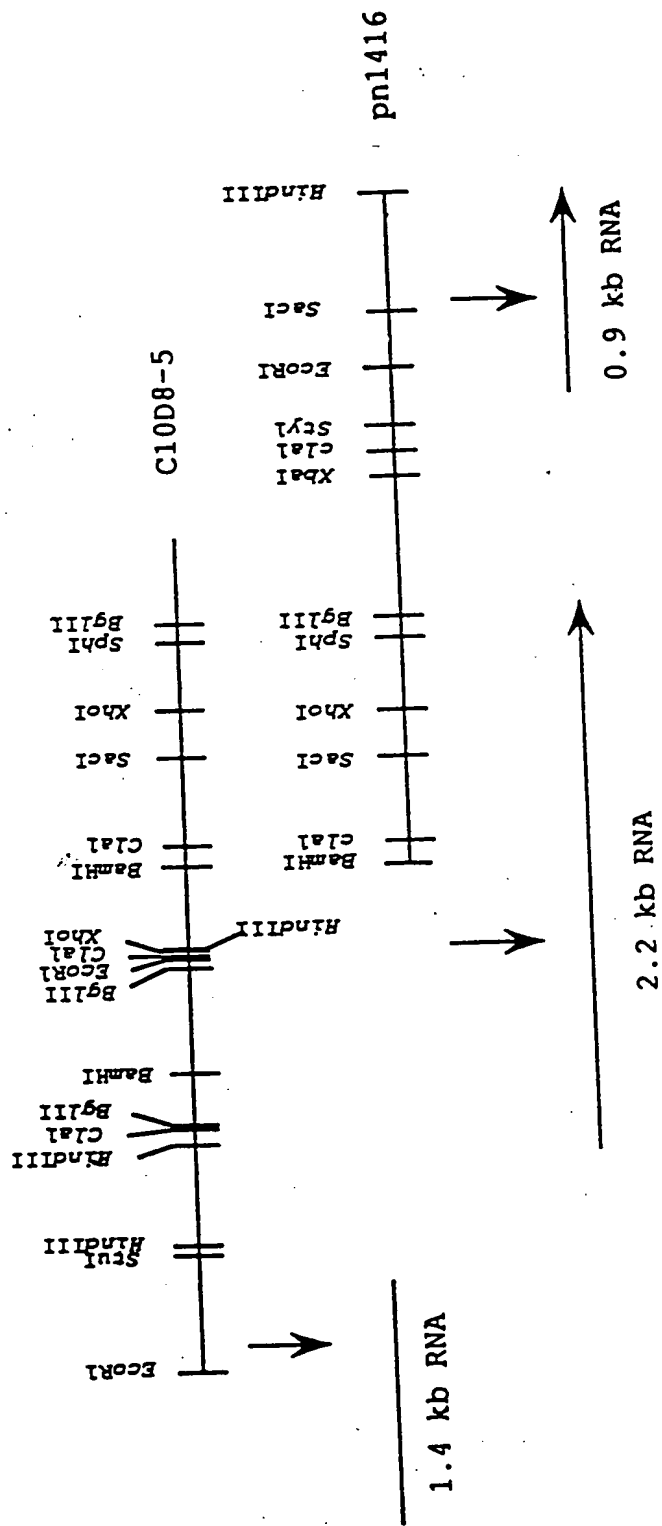


FIGURE 8

IV

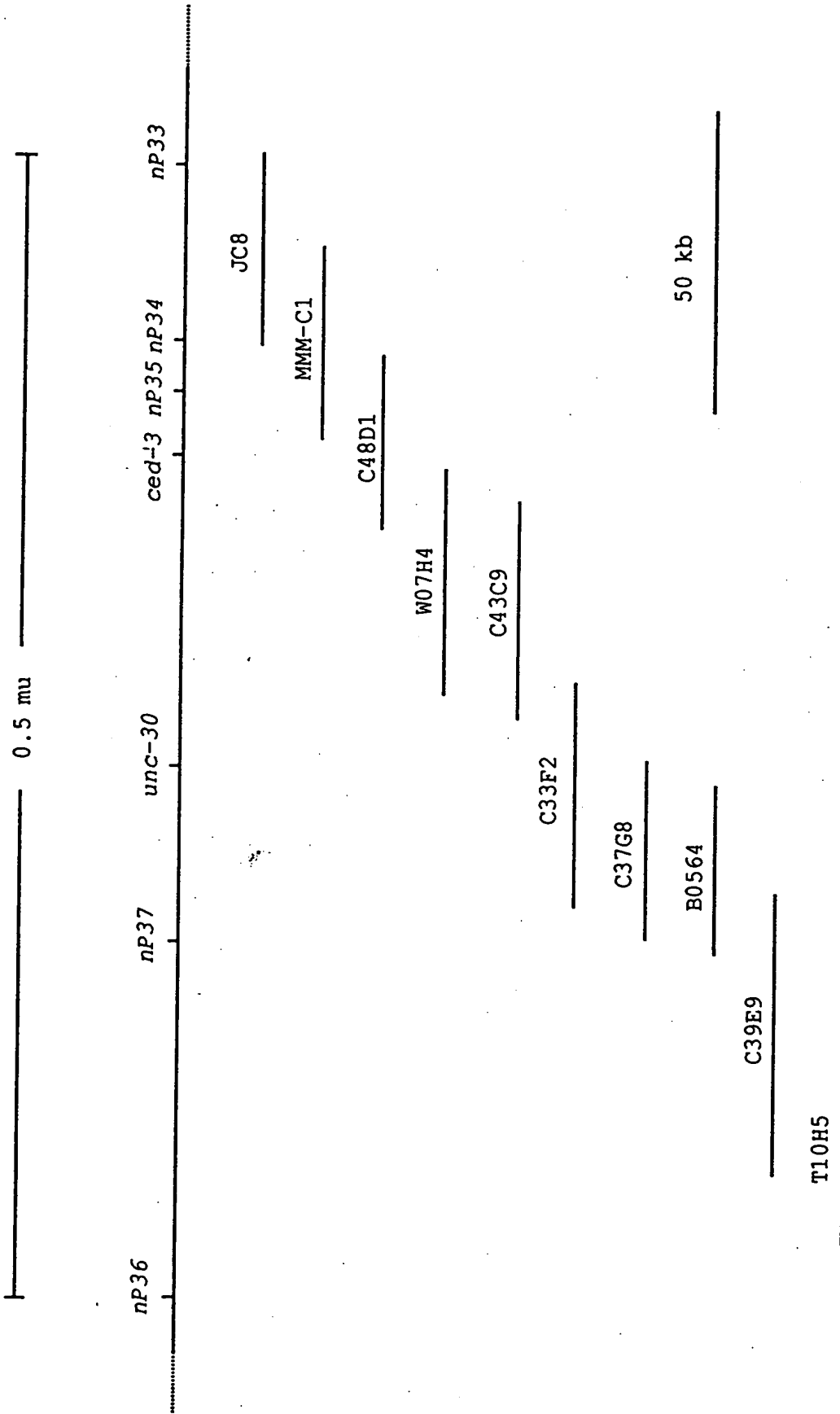


FIGURE 9

Figure 10 Summary of the experiments to localize *ced-3* gene within C48D1.

